

<210> 7  
<211> 22  
<212> DNA  
<213> Homo sapiens

<400> 7  
gcaagggtgc atcagtgtaa ga

22

<210> 8  
<211> 20  
<212> DNA  
<213> Homo sapiens

<400> 8  
tcccaccatc attcaacaaa

20

<210> 9  
<211> 26  
<212> DNA  
<213> Homo sapiens

<400> 9  
tccaataatt caccgggatc tgaagg

26

BEST AVAILABLE COPY

- 1/5 -

Fig. 1

atgaagaagt	tctctcggat	gcccagtgctg	gagggcgccga	gcggcgccgg	agcgcgccgg	60
ggcggggctg	gcggggccgg	ggccggggcc	ggctgcggct	ccggcgccctc	gtccgtgggg	120
gtccgggtgt	tcgcggtcgg	ccgccaccag	gtcaccctgg	aagagtcgct	ggccgaagg	180
ggattctcca	cagttttcct	cgtgcgtact	cacgggtgaa	tccgatgtgc	attgaagcga	240
atgtatgtca	ataacatgcc	agacctcaat	gtttgtaaaa	gggaaattac	aattatgaaa	300
gagctatctg	gtcacaaaaa	tattgtgggc	tatttggaact	gtgctgttaa	ttcaattagt	360
gataatgtat	gggaagtcct	tatcttaatg	gaatattgtc	gagctggaca	ggtagtgaat	420
caaatgaata	agaagctaca	gacgggtttt	acagaaccag	aagtgttaca	gatattctgt	480
gatacctgtg	aagctgttgc	aaggttgcac	cagtgtgaag	ctccaataat	tcaccgggat	540
ctgaaggtag	aaaatatatt	gttgaatgat	gggtgggaact	atgtactttg	tgactttggc	600
agtgccacta	ataaatttct	taactctcaa	aaagatggag	ttaatgtagt	agaagaagaa	660
attaaaaagt	atacaactct	gtcatacaga	gccccgaaa	tgatcaacct	ttatggaggg	720
aaacccatca	ccaccaaggc	tgatatctgg	gcactgggat	gtctactcta	taaaactttgt	780
ttcttcactc	ttccttttgg	tgagagtcag	gttgctatct	gtgatggcaa	cttcaccatc	840
ccagacaatt	ctcgttactc	ccgtaacata	cattgcttaa	taagggttcat	gcttgaacca	900
gatccggaac	atagacctga	tatatttcaa	gtgtcatatt	ttgcatthaa	atttgccaaa	960
aaggattgtc	cagtcctcaa	catcaataat	tcttctattc	cttcagctct	tcctgaaccg	1020
atgactgcta	gtgaagcagc	tgctaggaaa	agccaaataa	aagccagaat	aacagatacc	1080
attggacca	cagaaacctc	aattgcacca	agacaaagac	caaaggccaa	ctctgctact	1140
actgccactc	ccagtgtgct	gaccattcaa	agttcagcaa	cacctgttaa	agtccttgct	1200
cctgggtgaat	tcggtaacca	tagacaaaaa	ggggcactaa	gacctggaaa	tggccctgaa	1260
atthttattg	gtcagggacc	tcctcagcag	ccggccacagc	agcatagagt	actccagcaa	1320
ctacagcagg	gagattggag	attacagcaa	ctccatttac	agcatcgtca	tcctcaccag	1380
cagcagcagc	agcagcagca	gcaacagcaa	cagcagcagc	agcaacagca	acagcagcag	1440
cagcagcagc	agcagcagca	ccaccaccac	caccaccacc	acctacttca	agatgcttat	1500
atgcagcagt	atcaacatgc	aacacagcag	caacagatgc	ttcaacaaca	atthtttaatg	1560
cattcggtat	atcaaccaca	accttctgca	tcacagtatc	ctacaatgat	gccgcagtat	1620
cagcaggctt	tctttcaaca	gcagatgcta	gtctcaacatc	agccgtctca	acaacaggca	1680
tcacctghat	atcttacctc	ccctcaagag	ttctcaccag	ccttagtttc	ctacacttca	1740
tcacttccag	ctcaggttgg	aaccataatg	gactcctcct	atagtgccaa	taggcaagta	1800
tttttccagt	cagttgctga	taaagaggcc	attgcaaatt	tcacaaatca	gaagaacatc	1860
agcaatccac	ctgatatgtc	aggggtggaat	ccttttggag	aggataaatt	ctctaagtta	1920
acagaagagg	aactattgga	cagagaattt	gaccttctca	gatcaaatag	gctcaggagg	1980
agagcatcct	cagataagaa	tgtagactca	ctttctgctc	cacataacca	tcctccagaa	2040
gatccttttg	gttctgttcc	tttcatttct	cattcaggca	aggggttctcc	tgaaaagaaa	2100
gctgaacatt	catctataaa	tcaagaaaat	ggcactgcaa	accctatcaa	gaacggtaaa	2160
acaagtccag	catctaaaga	tcagcggact	ggaaagaaaa	cctcagtaca	gggtcaagtg	2220
caaaagggga	atgatgaatc	tgaaagtgat	tttgaatcag	atcccccttc	tcctaagagc	2280
agtgaagagg	aagagcaaga	tgatgaagaa	gttcttcagg	gggaacaagg	agattttaat	2340
gatgatgata	ctgaaccaga	aaatctgggt	ctataggcctc	tcctcatgga	ttctgaagat	2400
gaggaagaag	aggagaaaca	tagctctgat	tctgattatg	agcaggctaa	agcaaagtac	2460
agtgacatga	gctctgtcta	cagagacaga	tctggcagtg	gaccaacca	agatcttaat	2520
acaatactcc	tcacctcagc	ccaattatcc	tctgatgttg	cagtggagac	tcccaaacag	2580
gagttttagt	tatttggcgc	tgtccccctc	tttgcaagtgc	gtgctcaaca	gccccagcaa	2640
gaaaagaatg	aaaagaacct	ccctcaacac	aggtttctctg	ctgcaggact	ggagcaggag	2700
gaattttagt	tattcacaaa	ggcgcccttt	agcaagaagg	tgaatgtaca	agaatgccat	2760
gcagtggggc	ctgaggcaca	tactatccct	ggttatccca	aaagtgtaga	tgtatttggc	2820
tccactccat	ttcagccctt	cctcacatca	acaagtaaaa	gtgaaagcaa	tgaggacctt	2880
tttgggcttg	tgccctttga	tgaaataacg	gggagccagc	agcaaaaagt	caaacagcgc	2940
agcttacaga	aactgtcctc	tcgccaagg	cgcacaaagc	aggatatgtc	caaaagtaat	3000
gggaagcggc	atcatggcac	gccaactagc	acaaagaaga	ctttgaagcc	tacctatcgc	3060
actccagaga	gggctcgcag	gcacaaaaaa	gtgggcccgc	gagactctca	aagtagcaat	3120
gaatttttaa	ccatctcaga	ctccaaggag	aacattagtg	ttgacttgac	tgatgggaaa	3180
gataggggga	atgtcttaca	acctgaggag	agcctgttgg	accccttcgg	tgccaagccc	3240
ttccattctc	cagacctgtc	atggcaccct	ccacatcagg	gcctgagcga	catccgtgct	3300
gatcacaata	ctgtcctgcc	agggcgccca	agacaaaatt	cactacatgg	gtcatttccat	3360
agtgcagatg	tattgaaaat	ggatgatttt	ggtgccgtgc	cctttacaga	acttgtgtgt	3420
caaagcatca	ctccacatca	gtcccaacag	tcccaaccag	tcgaattaga	cccatttggg	3480
gctgctccat	ttcctttctaa	acagtag				3507



- 3/5 -

Fig. 2 (continued)

Gln	Gln	Gln	Gln	Gln	Gln	His	His	His	His	His	His	His	His	His	Leu	Leu
				485					490						495	
Gln	Asp	Ala	Tyr	Met	Gln	Gln	Tyr	Gln	His	Ala	Thr	Gln	Gln	Gln	Gln	Gln
			500					505						510		
Met	Leu	Gln	Gln	Gln	Phe	Leu	Met	His	Ser	Val	Tyr	Gln	Pro	Gln	Pro	
		515					520					525				
Ser	Ala	Ser	Gln	Tyr	Pro	Thr	Met	Met	Pro	Gln	Tyr	Gln	Gln	Ala	Phe	
	530					535					540					
Phe	Gln	Gln	Gln	Met	Leu	Ala	Gln	His	Gln	Pro	Ser	Gln	Gln	Gln	Ala	
545					550					555					560	
Ser	Pro	Glu	Tyr	Leu	Thr	Ser	Pro	Gln	Glu	Phe	Ser	Pro	Ala	Leu	Val	
			565						570					575		
Ser	Tyr	Thr	Ser	Ser	Leu	Pro	Ala	Gln	Val	Gly	Thr	Ile	Met	Asp	Ser	
		580						585					590			
Ser	Tyr	Ser	Ala	Asn	Arg	Gln	Val	Phe	Phe	Gln	Ser	Val	Ala	Asp	Lys	
	595					600						605				
Glu	Ala	Ile	Ala	Asn	Phe	Thr	Asn	Gln	Lys	Asn	Ile	Ser	Asn	Pro	Pro	
	610					615					620					
Asp	Met	Ser	Gly	Trp	Asn	Pro	Phe	Gly	Glu	Asp	Asn	Phe	Ser	Lys	Leu	
625					630					635					640	
Thr	Glu	Glu	Glu	Leu	Leu	Asp	Arg	Glu	Phe	Asp	Leu	Leu	Arg	Ser	Asn	
			645						650					655		
Arg	Leu	Glu	Glu	Arg	Ala	Ser	Ser	Asp	Lys	Asn	Val	Asp	Ser	Leu	Ser	
		660						665					670			
Ala	Pro	His	Asn	His	Pro	Pro	Glu	Asp	Pro	Phe	Gly	Ser	Val	Pro	Phe	
	675						680					685				
Ile	Ser	His	Ser	Gly	Lys	Gly	Ser	Pro	Glu	Lys	Lys	Ala	Glu	His	Ser	
	690					695					700					
Ser	Ile	Asn	Gln	Glu	Asn	Gly	Thr	Ala	Asn	Pro	Ile	Lys	Asn	Gly	Lys	
705					710					715					720	
Thr	Ser	Pro	Ala	Ser	Lys	Asp	Gln	Arg	Thr	Gly	Lys	Lys	Thr	Ser	Val	
			725						730					735		
Gln	Gly	Gln	Val	Gln	Lys	Gly	Asn	Asp	Glu	Ser	Glu	Ser	Asp	Phe	Glu	
		740					745						750			
Ser	Asp	Pro	Pro	Ser	Pro	Lys	Ser	Ser	Glu	Glu	Glu	Glu	Gln	Asp	Asp	
	755					760						765				
Glu	Glu	Val	Leu	Gln	Gly	Glu	Gln	Gly	Asp	Phe	Asn	Asp	Asp	Asp	Thr	
	770				775						780					
Glu	Pro	Glu	Asn	Leu	Gly	His	Arg	Pro	Leu	Leu	Met	Asp	Ser	Glu	Asp	
785					790					795					800	
Glu	Glu	Glu	Glu	Glu	Lys	His	Ser	Ser	Asp	Ser	Asp	Tyr	Glu	Gln	Ala	
			805						810					815		
Lys	Ala	Lys	Tyr	Ser	Asp	Met	Ser	Ser	Val	Tyr	Arg	Asp	Arg	Ser	Gly	
		820						825					830			
Ser	Gly	Pro	Thr	Gln	Asp	Leu	Asn	Thr	Ile	Leu	Leu	Thr	Ser	Ala	Gln	
	835						840					845				
Leu	Ser	Ser	Asp	Val	Ala	Val	Glu	Thr	Pro	Lys	Gln	Glu	Phe	Asp	Val	
	850					855					860					
Phe	Gly	Ala	Val	Pro	Phe	Phe	Ala	Val	Arg	Ala	Gln	Gln	Pro	Gln	Gln	
865					870					875					880	
Glu	Lys	Asn	Glu	Lys	Asn	Leu	Pro	Gln	His	Arg	Phe	Pro	Ala	Ala	Gly	
		885							890					895		
Leu	Glu	Gln	Glu	Glu	Phe	Asp	Val	Phe	Thr	Lys	Ala	Pro	Phe	Ser	Lys	
		900						905					910			
Lys	Val	Asn	Val	Gln	Glu	Cys	His	Ala	Val	Gly	Pro	Glu	Ala	His	Thr	
	915						920					925				
Ile	Pro	Gly	Tyr	Pro	Lys	Ser	Val	Asp	Val	Phe	Gly	Ser	Thr	Pro	Phe	
	930					935					940					
Gln	Pro	Phe	Leu	Thr	Ser	Thr	Ser	Lys	Ser	Glu	Ser	Asn	Glu	Asp	Leu	
945					950					955					960	

BEST AVAILABLE COPY

- 4/5 -

Fig. 2 (continued)

Phe	Gly	Leu	Val	Pro	Phe	Asp	Glu	Ile	Thr	Gly	Ser	Gln	Gln	Gln	Lys
				965					970					975	
Val	Lys	Gln	Arg	Ser	Leu	Gln	Lys	Leu	Ser	Ser	Arg	Gln	Arg	Arg	Thr
			980					985					990		
Lys	Gln	Asp	Met	Ser	Lys	Ser	Asn	Gly	Lys	Arg	His	His	Gly	Thr	Pro
		995					1000					1005			
Thr	Ser	Thr	Lys	Lys	Thr	Leu	Lys	Pro	Thr	Tyr	Arg	Thr	Pro	Glu	Arg
	1010					1015					1020				
Ala	Arg	Arg	His	Lys	Lys	Val	Gly	Arg	Arg	Asp	Ser	Gln	Ser	Ser	Asn
1025					1030					1035					1040
Glu	Phe	Leu	Thr	Ile	Ser	Asp	Ser	Lys	Glu	Asn	Ile	Ser	Val	Ala	Leu
				1045					1050					1055	
Thr	Asp	Gly	Lys	Asp	Arg	Gly	Asn	Val	Leu	Gln	Pro	Glu	Glu	Ser	Leu
		1060					1065					1070			
Leu	Asp	Pro	Phe	Gly	Ala	Lys	Pro	Phe	His	Ser	Pro	Asp	Leu	Ser	Trp
	1075						1080					1085			
His	Pro	Pro	His	Gln	Gly	Leu	Ser	Asp	Ile	Arg	Ala	Asp	His	Asn	Thr
	1090					1095					1100				
Val	Leu	Pro	Gly	Arg	Pro	Arg	Gln	Asn	Ser	Leu	His	Gly	Ser	Phe	His
1105				1110					1115						1120
Ser	Ala	Asp	Val	Leu	Lys	Met	Asp	Asp	Phe	Gly	Ala	Val	Pro	Phe	Thr
				1125					1130					1135	
Glu	Leu	Val	Val	Gln	Ser	Ile	Thr	Pro	His	Gln	Ser	Gln	Gln	Ser	Gln
		1140					1145					1150			
Pro	Val	Glu	Leu	Asp	Pro	Phe	Gly	Ala	Ala	Pro	Phe	Pro	Ser	Lys	Gln
	1155						1160					1165			

Fig. 2

cgggccaggg	gcgggcgaccc	ctcgcggaag	cccgggctg	cgccggggccg	gggacttgcc	60
cttgacgct	ccctgcgccc	tccagctcgc	cggcggggacc	atgaagaagt	tctctcggat	120
gcccagtcg	gagggcgcca	gcggcgggcg	agcgcggggt	ggcggggctg	gcggggccgg	180
ggcgggggcc	ggctgcggct	ccggcgggctc	gtccgtgggg	gtccgggtgt	tcgcggtcgg	240
ccgccaccag	gtcaccctgg	aagagtcgct	ggccgaaggt	ggattctcca	cagttttcct	300
cgtgcgtact	cacgggtgaa	tccgatgtgc	attgaagcga	atgtatgtca	ataacatgcc	360
agacctcaat	gtttgtaaaa	gggaaattac	aattatgaaa	gagctatctg	gtcacaaaaa	420
tattgtgggc	tatttggaact	gtgctgttaa	ttcaattagt	gataatgtat	gggaagtcct	480
tatcttaagt	gaatattgtc	gagctggaca	ggtagtgaat	caaatagaata	agaagctaca	540
gacgggtttt	acagaaccag	aagtgttaca	gatattctgt	gatacctgtg	aagctgttgc	600
aagggttgc	cagtgtgaaga	ctccaataat	tcaccgggat	ctgaaggtag	aaaatatttt	660
gttgaatgat	ggtgggaact	atgtactttg	tgactttggc	agtgcacta	ataaatttct	720
taatcctcaa	aaagatggag	ttaatgtagt	agaagaagaa	attaaaaagt	atacaactct	780
gtcatacaga	gcccctgaaa	tgatcaacct	ttatggaggg	aaacccatca	ccaccaaggc	840
tgatatctgg	gcactgggat	gtctactcta	ttaactttgt	ttcttcactc	ttccttttgg	900
tgagagtcag	gttgctatct	gtgatggcaa	cttcaccatc	ccagacaatt	ctcgttactc	960
ccgtaacata	cattgcttaa	taaggttcat	gcttgaacca	gatccggaac	atagacctga	1020
tatatattcaa	gtgtcatatt	ttgcatttaa	atttgccaaa	aaggattgtc	cagtctccaa	1080
catcaataat	tcttctattc	cttcagctct	tcctgaaccg	atgactgcta	gtgaagcagc	1140
tgctaggaaa	agccaaataa	aagccagaat	aacagatacc	attggaccaa	cagaaacctc	1200
aattgcacca	agacaaagac	caaaggccaa	ctctgctact	actgccactc	ccagtgtgct	1260
gaccattcaa	agttcagcaa	cacctgttaa	agtccttact	cctgggtgaat	tcggtaacca	1320
tagaccaaaa	ggggcactaa	gacctggaaa	tggccctgaa	attttattgg	gtcagggacc	1380
tcctcagcag	ccgccacagc	agcatagagt	actccagcaa	ctacagcagg	gagattggag	1440
attacagcaa	ctccatttac	agcatcgta	tcctcaccag	cagcagcagc	agcagcagca	1500
gcaacagcaa	cagcagcagc	agcaacagca	acagcagcag	cagcagcagc	agcagcagca	1560
ccaccaccac	caccaccacc	acctacttca	agatgcttat	atgcagcagt	atcaactatc	1620
aacacagcag	caacagatgc	ttcaacaaca	atttttaatg	cattcggtat	atcaaccaca	1680
accttctgca	tcacagtatc	ctacaatgat	gccgcagtat	cagcaggctt	tctttcaaca	1740
gcagatgcta	gctcaacatc	agccgtctca	acaacaggca	tcacctgaat	atcttacctc	1800

BEST AVAILABLE COPY

- 5/5 -

Fig. 3 (continued)

ccctcaagag	ttctcaccag	ccttagtttc	ctacacttca	tcacttccag	ctcaggttgg	1860
aaccataatg	gactcctcct	atagtgccaa	taggcaagta	tttttccagt	cagttgctga	1920
taaagaggcc	attgcaaatt	tcacaaatca	gaagaacatc	agcaatccac	ctgatatgtc	1980
agggtggaat	ccttttgag	aggataat	ctctaagtta	acagaagagg	aactattgga	2040
cagagaat	gaccttctaa	gatcaaatag	gctcgaggag	agagcatcct	cagataagaa	2100
tgtagactca	ccttctgtc	cacataacca	tcctccagaa	gatccttttg	gttctgttcc	2160
tttcatttct	cattcaggca	agggttctcc	tgaaaaga	gctgaacatt	catctataaa	2220
tcaagaaaat	ggcactgcaa	accctatcaa	gaacggtaaa	acaagtccag	catctaaaga	2280
tcagcggact	ggaaagaaaa	cctcagtaca	gggtcaagt	caaaagggga	atgatgaatc	2340
tgaaagtgat	tttgaatcag	atcccccttc	tcctaagagc	agtgaagagg	aagagcaaga	2400
tgatgaagaa	gttcttcagg	gggaacaagg	agattttaat	gatgatgata	ctgaaccaga	2460
aaatctgggt	cataggcctc	tcctcatgga	ttctgaagat	gaggaagaag	aggagaaaca	2520
tagctctgat	tctgattatg	agcaggctaa	agcaaagtac	agtgacatga	gctctgtcta	2580
cagagacaga	tctggcagtg	gaccaaccca	agatctta	acaatactcc	tcacctcagc	2640
ccaattatcc	tctgatgttg	cagtggagac	tcccaaacag	gagtttgatg	tatttggcgc	2700
tgtccccttc	tttgagctgc	gtgctcaaca	gccccagcaa	gaaaagaatg	aaaagaacct	2760
ccctcaacac	aggtttctcg	ctgcaggact	ggagcaggag	gaatttgatg	tattcacaaa	2820
ggcgctttt	agcaagaagg	tgaatgtaca	agaatgccat	gcagtggggc	ctgaggcaca	2880
tactatccct	ggttatccca	aaagtgtaga	tgtatttggc	tccactccat	ttcagccctt	2940
cctcacatca	acaagtaaaa	gtgaaagcaa	tgaggacctt	tttgggcttg	tgccctttga	3000
tgaaataacg	gggagccagc	agcaaaaagt	caaacagcgc	agcttacaga	aactgtcctc	3060
tcgccaaaagg	cgcacaaagc	aggatatgtc	caaaagta	gggaagcggc	atcatggcac	3120
gccaaactagc	acaaagaaga	ccttgaagcc	tacctatcgc	actccagaga	gggctcgcag	3180
gcacaaaaaa	gtgggcccgc	gagactctca	aagtagcaat	gaatttttaa	ccatctcaga	3240
ctccaaggag	aacattagtg	ttgcactgac	tgatgggaaa	gataggggga	atgtcttaca	3300
acctgaggag	agcctgttgg	accccttcgg	tgccaagccc	ttccattctc	cagacctgtc	3360
atggcaccct	ccacatcagg	gcctgagcga	catccgtgct	gatcacaata	ctgtcctgcc	3420
aggcgcgcca	agacaaaatt	cactacatgg	gtcattccat	agtgcagatg	tattgaaaat	3480
ggatgatttt	gggtgccgtg	cctttacaga	acttgtggtg	caaagcatca	ctccacatca	3540
gtcccaacag	tcccaaccag	tcgaattaga	cccatttgg	gctgtccat	ttccttctaa	3600
acagtagata	cttctgatgg	attctcggca	ttaactcctg	tttcaaaaaa	gtgtgaacag	3660
ttttatgaat	ttgaaagaaa	atttggtagc	tctttatagc	attc		3704

Fig. 4

```

>SEQDB|205286|38772 LBRI_1047_AA
MKKFSRMPKSEGGSGGGAAGGGAGGAGAGCGSGGSSVGVRVFAVGRHQ
VTLEESLAEGGFSTVFLVRTHGGIRCALKRMYVNNMPDLNVCKREITIMK
ELSGHKNI VGYLDCAVNSISDNVWEVLILMEYCRAGQVNVQMNKKLQTGF
TEPEVLQIFCDTCEAVARLHQCKTPIIHRDLKVENILLNDGGNYVLCDFG
SATNKF LNPQKDG VNVVEEIKKYTTL SYRAPEMINLYGGKPITTKADIW
ALGCLLYKLCFFTL PFGESQVAICDGNFTIPDNSRYSRNIHCLIRFMLEP
DPEHRPDI FQVSYFAFKFAKDCPVSNNINSSIPSALPEPMTASEAAARK
S QIKARITDTIGPTETS IAPRQRPKANSATTATPSVLT IQSSATPVKVLA
PGEFGNHRPKGALRPGNGPEILLGQGPPQPPQQHRVLQQLQGGDWRLQQ
LHLQHRHPHQQQQQQQQQQQQQQQQQQQQQQQQH HHHHHHHHLLQDAY
MQQYQHATQQQOMLQQQFLMHSVYQPPQPSASQYPTMMPQYQQAFFQQQML
AQHQPSQQQASPEYLTSPQEFSPALVSYTSSLPAQVGTIMDSSYSANRQV
FFQSVADKEAIANFTNQKNISNPPDMSGWNPFGE DNFSKLT EEEELLDREF
DLLRSNRL EERASSDKNVDLSAPHNHPPEDPFGSVVPFISHSGKGSPEKK
AEHSSINQENG TANPIKNGKTS PASKDQRTGKKT SVQGVQKGNDESESD
FESDPPSPKSSEEEEQDDEEVLQGEQGFND DDT E PENL GHRPLLMDSED
EEEEEEKHSSDS DYEQAKAKYSDMSSVYRDRSGSGPTQDLNTILL TSAQLS
SDVAVETPKQEFDFVFGAVPFFAVRAQQPQKEKNEKNLPQHRFPAAGLEQE
EFDVFTKAPFSKKVNVQECHAVGPEAHTIPGYPKSVDFGSTPFPQFLT S
TSKVESNEDLFG LVPFDEITGSQQQKVQRSLQKLSSRQRRTKQDMSKSN
GKRHHGTPTSTKKT LKPTYRTPERARRHKKVGRDRS QSSNEFLTISDSKE
NISVALTDGKDRGNVLQPEESLLDPFGAKPFHSPDLSWHPPHQGLSDIRA
DHNTVLPGRPRQNSLHGSFHSADVLKMDDFGAVPFTLVVQSITPHQSQQ
SQPVELDPFGAAPFPFSKQ

```

BEST AVAILABLE COPY